Typically, the first 18 nucleotides of the 5' end of these oligonucleotides contained annealing sites for the sequencing primers. Thus, the total product of the PCR reaction from an empty vector was 343 bp. However, signal sequence-fused cDNA resulted in considerably longer nucleotide sequences.

Following the PCR, an aliquot of the reaction (5 μl) was examined by agarose gel electrophoresis in a 1% agarose gel using a Tris-Borate-EDTA (TBE) buffering system as described by Sambrook et al., supra. Clones resulting in a single strong PCR product larger than 400 bp were further analyzed by DNA sequencing after purification with a 96 Qiaquick PCR clean-up column (Qiagen Inc., Chatsworth, CA).

EXAMPLE 3: Isolation of cDNA Clones Encoding Human PRO213

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA28735. Based on the DNA28735 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO213.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-TGGAGCAGCAATATGCCAGCC-3' (SEQ ID NO:3)

reverse PCR primer 5'-TTTTCCACTCCTGTCGGGTTGG-3' (SEQ ID NO:4)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA28735 sequence which had the following nucleotide sequence

hybridization probe

5'-GGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGG-3' (SEQ ID NO:5)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO213 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal lung tissue.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO213 [herein designated as UNQ187 (DNA30943-1163)] (SEQ ID NO:1) and the derived protein sequence for PRO213.

The entire nucleotide sequence of UNQ187 (DNA30943-1163) is shown in Figure 1 (SEQ ID NO:1). Clone UNQ187 (DNA30943-1163) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 336-338 and ending at the stop codon at nucleotide positions 1221-1223 (Figure 1). The predicted polypeptide precursor is 295 amino acids long (Figure 2). Clone UNQ187 (DNA30943-1163) has been deposited with ATCC.

Analysis of the amino acid sequence of the full-length PRO213 polypeptide suggests that a portion of it possesses significant homology to the human growth arrest-specific gene 6 protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO213 amino acid sequence and the following Dayhoff sequences, HSMHC3W5A_6 and B48089.

EXAMPLE 4: Isolation of cDNA Clones Encoding Human PRO274

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA36469. Based on the DNA36469 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO274. ESTs proprietary to Genentech were employed in the consensus assembly. The ESTs are shown in Figures 5-7 and are herein designated DNA17873, DNA36157 and DNA28929, respectively.

Pairs of PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 (36469.f1) 5'-CTGATCCGGTTCTTGGTGCCCCTG-3' (SEQ ID NO:11)

forward PCR primer 2 (36469.f2) 5'-GCTCTGTCACTCACGCTC-3' (SEQ ID NO:12)

forward PCR primer 3 (36469.f3) 5'-TCATCTCTTCCCTCTCCC-3' (SEQ ID NO:13)

forward PCR primer 4 (36469.f4) 5'-CCTTCCGCCACGGAGTTC-3' (SEQ ID NO:14)

reverse PCR primer 1 (36469.r1) 5'-GGCAAAGTCCACTCCGATGATGTC-3' (SEQ ID NO:15)

reverse PCR primer 2 (36469.r2) 5'-GCCTGCTGTGGTCACAGGTCTCCG-3' (SEQ ID NO:16)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA36469 sequence which had the following nucleotide sequence

hybridization probe (36469.p1)

5'-TCGGGGAGCAGGCCTTGAACCGGGGCATTGCTGCTGTCAAGGAGG-3' (SEQ ID NO:17)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO274 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal liver tissue (LIB229).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO274 [herein designated as UNQ241 (DNA39987-1184)] (SEQ ID NO:1) and the derived protein sequence for PRO274.

The entire nucleotide sequence of UNQ241 (DNA39987-1184) is shown in Figure 3 (SEQ ID NO:6). Clone UNQ241 (DNA39987-1184) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 83-85 and ending at the stop codon at nucleotide positions 1559-1561 (Figure 3). The predicted polypeptide precursor is 492 amino acids long (Figure 4), has an estimated molecular weight of about 54,241 daltons and an estimated pI of about 8.21. Clone UNQ241 (DNA39987-1184) has been deposited with ATCC and is assigned ATCC deposit no. 209786.

Analysis of the amino acid sequence of the full-length PRO274 polypeptide suggests that it possesses significant homology to the Fn54 protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO274 amino acid sequence and the following Dayhoff sequences, MMFN54S2_1, MMFN54S1_1, CELF48C1_8, CEF38B7_6, PRP3_RAT, INL3_PIG, MTCY07A7_13, YNAX_KLEAE, A47234 and HME2_MOUSE.

EXAMPLE 5: Isolation of cDNA Clones Encoding Human PRO300

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1

above, wherein the consensus sequence obtained is herein designated DNA35930. Based on the DNA35930 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO300.

Forward and reverse PCR primers were synthesized:

forward PCR primer 1 (35930.f1) 5'-GCCGCCTCATCTTCACGTTCTTCC-3' (SEQ ID NO:20)
forward PCR primer 2 (35930.f2) 5'-TCATCCAGCTGGTGCTGCTC-3' (SEQ ID NO:21)
forward PCR primer 3 (35930.f3) 5'-CTTCTTCCACTTCTGCCTGG-3' (SEQ ID NO:22)
forward PCR primer 4 (35930.f4) 5'-CCTGGGCAAAAATGCAAC-3' (SEQ ID NO:23)
reverse PCR primer 1 (35930.r1) 5'-CAGGAATGTAGAAGGCACCCACGG-3' (SEQ ID NO:24)
reverse PCR primer 2 (35930.r2) 5'-TGGCACAGATCTTCACCCACACGG-3' (SEQ ID NO:25)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35930 sequence which had the following nucleotide sequence

hybridization probe (35930.p1)
5'-TGTCCATCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG-3' (SEQ ID NO:26)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO300 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO300 [herein designated as UNQ263 (DNA40625-1189)] (SEQ ID NO:18) and the derived protein sequence for PRO300.

The entire nucleotide sequence of UNQ263 (DNA40625-1189) is shown in Figure 8 (SEQ ID NO:18). Clone UNQ263 (DNA40625-1189) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 45-47 and ending at the stop codon at nucleotide positions 1416-1418 (Figure 8). The predicted polypeptide precursor is 457 amino acids long (Figure 9). Clone UNQ263 (DNA40625-1189) has been deposited with ATCC and is assigned ATCC deposit no. 209788.

Analysis of the amino acid sequence of the full-length PRO300 polypeptide suggests that portions of it possess significant homology to the Diff 33 protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO300 amino acid sequence and the following Dayhoff sequence, HSU49188_1.

EXAMPLE 6: Isolation of cDNA Clones Encoding Human PRO284

Two cDNA sequences were isolated in the amylase screen described in Example 2 and those cDNA sequences are herein designated DNA12982 (see Figure 12; human placenta-derived) and DNA15886 (see Figure 13; human salivary gland-derived). The DNA12982 and DNA15886 sequences were then clustered and aligned, giving rise to a consensus nucleotide sequence herein designated DNA18832.

Based on the DNA18832 consensus sequence, oligonucleotide probes were generated and used to screen a human placenta library (LIB89) prepared as described in paragraph 1 of Example 2 above. The cloning vector